CLAIMS

What is claimed is:

1. An isolated nucleic acid fragment comprising a nucleotide sequence selected from the group consisting of (a) a nucleotide sequence corresponding to any of the nucleotide sequences set forth in SEQ ID NOS:1, 3, 5, 7 or 9 or the complement thereof, or (b) the nucleotide sequence of (a) wherein said sequence is degenerate in accordance with the degeneracy of the genetic code.

2. An isolated nucleic acid fragment comprising:

(a) the first nucleic acid fragment of Claim 1, and

(b) a second nucleic acid fragment encoding a plant cystathionine γ-synthase or a functionally equivalent subfragment thereof.

3. A chimeric gene comprising the isolated nucleic acid fragment of 1 operably linked to a regulatory sequence.

4. A nucleic acid fragment comprising

(a) the chimeric gene of claim 3, and

(b) a second chimeric gene comprising a nucleic acid fragment encoding a plant cystathionine γ-synthase or a functionally equivalent subfragment thereof or a complement thereof operably linked to a regulatory sequence.

5. A plant comprising in its genome the chimeric gene of Claim 3 or the nucleic acid fragment of Claim 4.

6. Seeds derived from the plant of Claim 5.

7. A transformed host cell comprising the chimeric gene of Claim 3 or the nucleic acid fragment of Claim 4.

8. The transformed host cell of Claim 7 wherein said host cell is selected from the group consisting of a plant cell and a microbial cell.

9. A polypeptide comprising all or a substantial portion of the amino acid sequence set forth in SEQ ID NOS:2, 4, 6, 8 and 10.

10. A method for increasing methionine content of the seeds of plants comprising:

(a) transforming plant cells with the chimeric gene of Claim 3 or the nucleic acid fragment of Claim 4;

(b) growing fertile mature plants from the untransformed plant cells obtained from step (a) under conditions suitable to obtain seeds; and

selecting progeny seed of step (b) for those seeds containing increased levels of methionine compared to untransformed seeds.

11. A method for producing plant methionine synthase comprising:

(a) transforming host cells with the chimeric gene of Claim 3 or the nucleic acid fragment of Claim 4;

(b) growing the transformed microbial cells obtained from step (a) under conditions that result in expression of a plant methionine synthase protein.

12. The method of Claim 11 wherein the host cell is a microbial cell.

13. A method for evaluating at least one compound for its ability to inhibit the activity of a plant methionine synthase, the method comprising the steps of:

(a) transforming a host cell with a chimeric gene comprising a nucleic acid fragment encoding a plant methionine synthase, operably linked to suitable regulatory sequences;

(b) growing the transformed host cell under conditions that are suitable for expression of the chimeric gene wherein expression of the chimeric gene results in production of the plant methionine synthase encoded by the operably linked nucleic acid fragment in the transformed host cell;

(c) optionally purifying the plant methionine synthase expressed by the transformed host cell;

(d) treating the plant methionine synthase with a compound to be tested; and

(e) comparing the activity of the plant methionine synthase that has been treated with a test compound to the activity of an untreated plant methionine synthase,

thereby selecting compounds with potential for inhibitory activity.

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